

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/905,558

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length.
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
.000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIFE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/905,558

DATE: 07/26/2001
TIME: 18:55:29

Input Set : A:\1016.SEQLIST.TXT
Output Set: N:\CRF3\07262001\I905558.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Garnaat, Carl W.
5 Lowe, Keith S.
6 Roth, Bradley A.
11 <120> TITLE OF INVENTION: ZmAxigl Polynucleotides and Methods of
12 Use
14 <130> FILE REFERENCE: 1016
16 <140> CURRENT APPLICATION NUMBER: US/09/905,558
16 <141> CURRENT FILING DATE: 2001-07-13
16 <150> PRIOR APPLICATION NUMBER: US 60/217,942
17 <151> PRIOR FILING DATE: 2000-07-13
19 <160> NUMBER OF SEQ ID NOS: 21
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

447 <210> SEQ ID NO: 20
448 <211> LENGTH: 622
449 <212> TYPE: DNA
450 <213> ORGANISM: Zea mays
452 <400> SEQUENCE: 20
453 gcatgaataa tccccaaaac cctaaagcca gtgctccttg caccttgcca cggagcttc 60
454 ccaaagaagc agtggcgacc gacgaagcac cgccgccaat gggcaacaac aacaacacgg 120
455 aatcgggcgc ggcgacgatg gtccgggagc aggaccggct gatgcccggt gccaacgtgt 180
E--> 456 cccgcatcat gcgccaagtg ctgcctccgt acgccaagat ctccgacgac gcccaagaag 240
E--> 457 tnatccaaga attgcttttc' ggaatttcac cacttcgctc ctggcgaggc gaaacgaagc 300
458 ggtgccacac cgagcgccgc aagaccgtca cctccgaaga catcgtgtgg gccatgagcc 360
E--> 459 gcctcggtct cgacgaactac gtgcgcgcc ctcggcgctt cctccagcgc atgcgcgacn 420
E--> 460 acagcgaaca cgggggtgaa aacgcggcgg cctgcanggg gtngtggtcn cgccgcgggt 480
E--> 461 cgtctncttg gcgtccctt gccgcaanag atgacaactt gcaccaaacy tctgccgggn 540
E--> 462 tcggacaaa actnttcctt gttgcaggaa taccgctcn gggccttcc cccccaatc 600
463 caaccatttg gtttccccctt gc 622
465 <210> SEQ ID NO: 21
466 <211> LENGTH: 65
467 <212> TYPE: PRT
468 <213> ORGANISM: Zea mays
470 <400> SEQUENCE: 21
E--> 471 Arg Glu Gln Asp Xaa Xaa Met Pro Ile Ala Asn Val Ile Arg Ile Met
472 1 5 10 15
E--> 473 Arg Xaa Xaa Leu Pro Xaa His Ala Lys Ile Ser Asp Asp Ala Lys Glu
474 20 25 30
E--> 475 Xaa Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Xaa Thr Xaa Glu
476 35 40 45
E--> 477 Ala Asn Xaa Arg Cys Xaa Xaa Xaa Xaa Arg Lys Thr Xaa Xaa Xaa Glu
478 50 55 60
E--> 479 Xaa
480 65

see
item 9
on Ena
summary
sheet

item 9

item 9

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/905,558

DATE: 07/26/2001

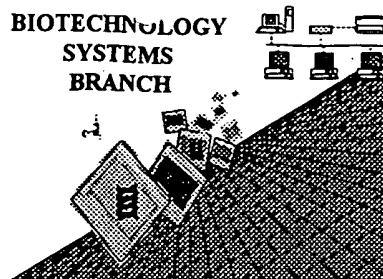
TIME: 18:55:30

Input Set : A:\1016.SEQLIST.TXT

Output Set: N:\CRF3\07262001\I905558.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:456 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
M:340 Repeated in SeqNo=20
L:471 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21
M:340 Repeated in SeqNo=21

RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/905,558

Source: O/PE

Date Processed by STIC: 7/26/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>